

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: CHOU, Tau-San

EISENREICH, Robert

SANFORD, John BLOWERS, Alan SMITH, Franzine VAN ECK, Joyce

- (ii) TITLE OF INVENTION: PRODUCTION OF TRANSGENIC POINSETTIA
- (iii) NUMBER OF SEQUENCES: 23
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Foley & Lardner
 - (B) STREET: 3000 K Street, N.W., Suite 500 (C) CITY: Washington

 - (D) STATE: D.C.
 - (E) COUNTRY: USA
 - (F) ZIP: 20007-5109
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible

 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/903,944
 (B) FILING DATE: 31-JUL-1997
 (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:

 - (A) NAME: GRANADOS, Patricia D.(B) REGISTRATION NUMBER: 33,683
 - (C) REFERENCE/DOCKET NUMBER: 89166/107
 - (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (202)672-5300
 - (B) TELEFAX: (202)672-5399
 - (C) TELEX: 904136
- (2) INFORMATION FOR SEQ ID NO:1:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
 - Gly Ile Gly Lys Phe Leu His Ser Ala Lys Lys Phe Gly Lys Ala Phe

Val Gly Glu Ile Met Asn Ser 20

- (2) INFORMATION FOR SEQ ID NO:2:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 amino acids

 - (B) TYPE: amino acid(C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Gly Met Ala Ser Lys Ala Gly Ala Ile Ala Gly Lys Ile Ala Lys Val

Ala Leu Lys Ala Leu 20

- (2) INFORMATION FOR SEQ ID NO:3:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Gly Ile Gly Lys Phe Leu Lys Ser Ala Lys Lys Phe Gly Lys Ala Phe

Val Lys Ile Leu Asn Ser

- (2) INFORMATION FOR SEQ ID NO:4:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 amino acids

 - (B) TYPE: amino acid (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Ala Gly Lys Ile Ala

- (2) INFORMATION FOR SEQ ID NO:5:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

	(xi)	SEQ	JENCI	E DES	SCRI	PTIO	N: S	EQ I	D NO	:5:							
	Lys 1	Arg	Lys	Arg	Ala 5	Val	Lys	Arg	Val	Gly 10	Arg	Arg	Leu	Lys	Lys 15	Leu	
	Ala	Arg	Lys	Ile 20	Ala	Arg	Leu	Gly	Val 25	Ala	Phe						
(2)	INFO	RMAT	ON E	FOR S	SEQ :	ID NO	0:6:										
	(i _.)	(B) (C)	LEN TYI STI	IGTH: PE: r RANDE	: 75 nucle EDNE:	TERIS base eic a SS: s linea	e pa: acid sing:	irs									
	(ix)		MAN	IE/KE		CDS 172	2										
	(ix)		NAM	IE/KE		mat_r 172		ide									
	(xi)	SEQU	JENCE	DES	CRI	PTION	1: SE	EQ II	ои о	:6:							
ATG Met 1	GGC . Gly	ATC G	GA A	AG I ys E 5	TTC (Phe I	CTT (Leu H	CAC A	AGT (Ser)	GCA A Ala 1 10	AAG A Lys I	AAG :	TTC (Phe (GGA A	AAG ys 15	GCC Ala		48
TTC Phe	GTG Val	GGT G	AG A lu I 20	TC A	ATG <i>I</i> let <i>I</i>	AAC A Asn S	AGT 1 Ser	ГАА									75
(2)	INFO	RMATI	ON F	or s	EQ 1	D NC):7:										
	(i) SE	(A) (B)	LENG TYPE	TH: : an	ACTER 24 a nino 7: li	minc ació	aci 1	ids								
	(i:	i) MO	LECU	LE T	YPE :	pro	tein	ı									
	(x:	i) SE	QUEN	CE D	ESCR	RIPTI	ON:	SEQ	ID N	10 : 7 :							
Met 1	Gly :	Ile G	ly L	ys P 5	he I	eu H	is S	Ser A	Ala I 10	ys L	ys I	he C	Sly L	ys 1 15	Ala		
Phe	Val (_	lu I 20	le M	let A	sn S	er										
(2)	INFO	RMATI	ON F	OR S	EQ I	D NO	:8:										
	(i)	(B)	LEN TYP STR	GTH: E: n ANDE	72 ucle DNES	ERIS base ic a S: s inea	pai cid ingl	rs									

	(A) NAME/KEY: CDS (B) LOCATION: 169	
	<pre>(ix) FEATURE: (A) NAME/KEY: mat_peptide (B) LOCATION: 169</pre>	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:	
ATG Met 1	GGA ATC GGC AAG TTC CTC AAG AGC GCA AAG AAG TTT GGC AAG GCC Gly Ile Gly Lys Phe Leu Lys Ser Ala Lys Lys Phe Gly Lys Ala 5 10 15	48
	GTG AAG ATC CTG AAC TCC TAA Val Lys Ile Leu Asn Ser 20	72
(2)	INFORMATION FOR SEQ ID NO:9:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 23 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: protein	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:	
Met 1	Gly Ile Gly Lys Phe Leu Lys Ser Ala Lys Lys Phe Gly Lys Ala 5 10 15	
Phe	Val Lys Ile Leu Asn Ser 20	
(2)	INFORMATION FOR SEQ ID NO:10:	
	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 69 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
	(ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 166	
	(ix) FEATURE: (A) NAME/KEY: mat_peptide (B) LOCATION: 166	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:	
ATG Met 1	AAG ATC GCC GGA AAG ATA GCA AAG ATT GCG GGG AAA ATC GCG AAG Lys Ile Ala Gly Lys Ile Ala Lys Ile Ala Gly Lys Ile Ala Lys 5 10 15	48
	GCT GGC AAA ATC GCG TAA Ala Gly Lys Ile Ala 20	69

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	(2)	INFORMATION FOR SEQ ID NO:11:	
		(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 22 amino acids(B) TYPE: amino acid(D) TOPOLOGY: linear	
		(ii) MOLECULE TYPE: protein	
		(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:	
•	Met 1	Lys Ile Ala Gly Lys Ile Ala Lys Ile Ala Gly Lys Ile Ala Lys 5 10 15	
	Ile	Ala Gly Lys Ile Ala 20	
	(2)	INFORMATION FOR SEQ ID NO:12:	
		(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 84 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
		(ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 181	
·		<pre>(ix) FEATURE: (A) NAME/KEY: mat_peptide (B) LOCATION: 181</pre>	
		(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:	
		AAG AGG AAG CGT GCA GTT AAG AGG GTG GGA CGT CGA TTG AAG CTT Lys Arg Lys Arg Ala Val Lys Arg Val Gly Arg Arg Leu Lys Leu 5 10 15	48
		AGA AAG ATC GCA AGG CTC GGT GTG GCT TTC TAA Arg Lys Ile Ala Arg Leu Gly Val Ala Phe 20 25	84
	(2)	INFORMATION FOR SEQ ID NO:13:	
		(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 27 amino acids(B) TYPE: amino acid(D) TOPOLOGY: linear	
		(ii) MOLECULE TYPE: protein	
		(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:	
	Met 1	Lys Arg Lys Arg Ala Val Lys Arg Val Gly Arg Arg Leu Lys Leu 5 10 15	
	Ala	Arg Lys Ile Ala Arg Leu Gly Val Ala Phe 20 25	

(2) INFORMATION FOR SEQ ID NO:14:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 120 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 1117	
<pre>(ix) FEATURE: (A) NAME/KEY: mat_peptide (B) LOCATION: 1117</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:	
ATG CTT CTC GCT ATT GCC TTC TTG GCA TCA GTT TGC GTG TCT TCC ATG Met Leu Leu Ala Ile Ala Phe Leu Ala Ser Val Cys Val Ser Ser Met 1 5 10 15	48
GGC ATC GGA AAG TTC CTT CAC AGT GCA AAG AAG TTC GGA AAG GCC TTC Gly Ile Gly Lys Phe Leu His Ser Ala Lys Lys Phe Gly Lys Ala Phe 20 25 30	96
GTG GGT GAG ATC ATG AAC AGT TAA Val Gly Glu Ile Met Asn Ser 35	20
(2) INFORMATION FOR SEQ ID NO:15:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 39 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: protein	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:	
Met Leu Leu Ala Ile Ala Phe Leu Ala Ser Val Cys Val Ser Ser Met 1 5 10 15	
Gly Ile Gly Lys Phe Leu His Ser Ala Lys Lys Phe Gly Lys Ala Phe 20 25 30	
Val Gly Glu Ile Met Asn Ser 35	
(2) INFORMATION FOR SEQ ID NO:16:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 111 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..108

	<pre>(ix) FEATURE: (A) NAME/KEY: mat_peptide (B) LOCATION: 1108</pre>	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:	
ATG Met 1	CTT CTC GCT ATT GCC TTC TTG GCA TCA GTT TGC GTG TCT TCC GGA Leu Leu Ala Ile Ala Phe Leu Ala Ser Val Cys Val Ser Ser Gly 5 10 15	48
ATG Met	GCC TCT AAG GCA GGT GCT ATC GCC GGC AAA ATC GCG AAG GTG GCA Ala Ser Lys Ala Gly Ala Ile Ala Gly Lys Ile Ala Lys Val Ala 20 25 30	96
	AAG GCC CTT TAA Lys Ala Leu 35	111
(2)	INFORMATION FOR SEQ ID NO:17:	
	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 36 amino acids(B) TYPE: amino acid(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: protein	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:	
Met 1	Leu Leu Ala Ile Ala Phe Leu Ala Ser Val Cys Val Ser Ser Gly 5 10 15	
Met	Ala Ser Lys Ala Gly Ala Ile Ala Gly Lys Ile Ala Lys Val Ala 20 25 30	
Leu	Lys Ala Leu 35	
(2)	INFORMATION FOR SEQ ID NO:18:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 117 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 1114	
	<pre>(ix) FEATURE: (A) NAME/KEY: mat_peptide (B) LOCATION: 1114</pre>	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:	
ATG Met 1	CTT CTC GCT ATT GCC TTC TTG GCA TCA GTT TGC GTG TCT TCC ATG Leu Leu Ala Ile Ala Phe Leu Ala Ser Val Cys Val Ser Ser Met 5 10 15	4.8

GGA Gly	ATC (GGC .	AAG Lys 20	TTC Phe	CTC Leu	AAG Lys	AGC Ser	GCA Ala 25	AAG Lys	AAG Lys	TTT Phe	GGC Gly	AAG Lys 30	GCC Ala	TTC Phe	96
	AAG . Lys					TAA										117
(2)	INFO	RMAT	ION	FOR	SEQ	ID N	10:19	€:								
	(i) S	(A) (B)	LEN TYI	IGTH PE: 8		amin ac:									
	(i	i) M	OLEC	CULE	TYPI	E: pi	rote	in								
	(x	i) S	EQUE	ENCE	DES	CRIP	rion	: SE	Q ID	NO:	19:					
Met 1	Leu	Leu	Ala	Ile 5	Ala	Phe	Leu	Ala	Ser 10	Val	Cys	Val	Ser	Ser 15	Met	
Gly	Ile	Gly	Lys 20	Phe	Leu	Lys	Ser	Ala 25	Lys	Lys	Phe	Gly	Lys 30	Ala	Phe	
Val	Lys	Ile 35	Leu	Asn	Ser											
(2)	INFC	RMAI	CION	FOR	SEQ	ID 1	NO:2	0:								
	(i)	(E	A) LI B) T C) S	ENGT YPE : IRAN	H: 1 nuc DEDN	CTER 11 ba leic ESS: lina	ase aci sin	pair d	s							
	(ix)		A) N.	AME/		CDS										
	(ix)		A) N.	AME/		mat 1		tide								
	(xi)	SEÇ	QUEN	CE D	ESCR	IPTI	ON:	SEQ	ID N	0:20	:					
ATG Met 1	CTT Leu	CTC Leu	GCT Ala	ATT Ile 5	Ala	TTC Phe	TTG Leu	GCA Ala	TCA Ser 10	Val	TGC Cys	GTG Val	TCT	TCC Ser 15	Lys	48
ATC Ile	GCC Ala	GGA Gly	AAG Lys 20	Ile	GCA Ala	AAG Lys	ATT Ile	GCG Ala 25	Gly	AAA	ATC	GCG Ala	AAG Lys 30	Ile	GCT Ala	96
	AAA Lys															111

(2)	INFORMA	TION	FOR	SEQ	ו ענ	NO : 2.	L:								
	(i)	(B)	ENCE LEN TYI TOI	NGTH PE: a	: 36 aming	amin o ac	no ao id								
	(ii)	MOLE	CULE	TYPI	E: p	rote:	in								
	(xi)	SEQUI	ENCE	DESC	CRIP	rion	: SEQ	O ID	NO:2	21:					
Met 1	Leu Leu	Ala	Ile 5	Ala	Phe	Leu	Ala	Ser 10	Val	Cys	Val	Ser	Ser 15	Lys	
Ile	Ala Gly	Lys 20	Ile	Ala	Lys	Ile	Ala 25	Gly	Lys	Ile	Ala	Lys 30	Ile	Ala	
Gly	Lys Ile 35														
(2)	INFORMA	TION	FOR	SEQ	ID 1	NO : 22	2:								
	(QUENC A) LI B) TY C) SY D) TO	ENGTI YPE : FRANI	i: 12 nucl DEDNI	29 ba leic ESS:	ase p acio sino	pairs i	5							
		ATURI A) NA B) LO	AME/I			126									
		ATURI A) NA B) LO	AME/I				ide								
	(xi) SE	QUEN	CE DI	ESCR	IPTIC	ON: S	SEQ :	D NO	0:22	:					
	CTT CTC Leu Leu														4:
	AAG CGT Lys Arg														91
	AAG ATC Lys Ile 35								TAA						12:
(2)	INFORMA	SEQUI (A) (B)		CHAI	RACTI : 42	ERIST amin	FICS: no ac								

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Met Leu Leu Ala Ile Ala Phe Leu Ala Ser Val Cys Val Ser Ser Lys
1 5 10 15

Arg Lys Arg Ala Val Lys Arg Val Gly Arg Arg Leu Lys Lys Leu Ala 20 25 30

Arg Lys Ile Ala Arg Leu Gly Val Ala Phe 35 40